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DEFINITION  AL522989, L1, NF1, cDNA, Homo sapiens cDNA clone CS01B009Y14.5
           prime, mRNA sequence.
ACCESSION   AL522989
VERSION     AL522989.1  GI:12792482
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 837)
AUTHORS     Li, W.R., Gruber, C., Jessee, J., and Polayes, D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqrel@genoscope.cns.fr, web: www.genoscope.cns.fr
FEATURES             Location/Qualifiers
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     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-poly(dT) primer. Five prime end
enriched, double stranded cDNA was digested with NotI and
cloned into the NotI and EcoRV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by life technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8371 Email: lliang@lifestech.com URL:
http://216.166.148.invitrogen.com"
BASE COUNT      199 a      241 c      229 g      177 t      1 others
ORIGIN
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56 rLeuTyAsnAspCysProGlyProGlyCysAspThrAspCysArg 73
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ACCESSION   AL521978
VERSION     AL521978.1  GI:10992332
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 761)
AUTHORS     Ota, T., Nishikawa, T., Suzuki, Y., Ishiguro, S., Goto, K., Kawai, Y.,
            Yamamoto, S., Wakamatsu, A., Nakamura, Y., Naito, T., Sugano, S., and
            Isoda, T.
TITLE       cDNA project
JOURNAL     Unpublished (2000)
COMMENT     Contact: Takao Isoda
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yama, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3951
            Fax: 81-438-52-3952
            Email: genomics@helix.jp
            HRI human cDNA project: 5'- & 3'- end are pass sequenced; Helix
            Research Institute; cDNA library construction; Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.
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PRIMER, mRNA sequence.
ACCESSION AL577008
VERSION AL577008.1 GI:12930716
KEYWORDS EST.

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SOURCE human.  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 975)  
 AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, web: www.genoscope.cns.fr.  
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 location/Qualifiers  
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 was primed with a NotI oligo(3T) primer. Five prime end  
 enriched, double-stranded cDNA was digested with NotI and  
 cloned into the NotI and EcoRV sites of the pCMVSPORT 6  
 vector. Library was normalized. Library was constructed by  
 life technologies. Contact: Feng Liang life technologies,  
 a division of invitrogen 9800 Medical Center drive  
 Rockville, Maryland 20850, USA Fax: (1) 301 610 8371  
 Email: fliang@lifestech.com URL: <http://lifestech.invitrogen.com>  
 BASIC COUNT 231 a 258 c 259 g 221 t 6 others  
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 Quality: 1074.50 Length: 211  
 Ratio: 5.482 Gaps: 2  
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prime, mRNA sequence.  
ACCESSION AL529836  
VERSION AL529836.1 G1:12793329  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 942)  
AUTHORS Li, W.H., Gruber, C., Josse, J., and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry - cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES  
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/note="Orqan: brain; Vector: pCMVSport 6; 1st strand cDNA was primed with a NotI clone(JR) primer. Five prime end enriched, double stranded cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSport 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a Division of Invitrogen 9800 Medical Center Drive, Folsom, CA 95630, USA Fax : (916) 301 613 8371 Email : fliang@lifestechn.com URL : http://f.fliang@lifestechn.com"

BASE COUNT 208 a 259 c 248 g 224 t 3 others  
ORIGIN

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Quality: 1064.50  
Ratio: 5.476  
Percent similarity: 93.96 Percent identity: 92.96  
alignment\_block:  
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prime, mRNA sequence.  
ACCESSION AL52021  
VERSION AL52021.1 G1:10947567  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 845)  
AUTHORS Nakamura, Y., Nishikawa, T., Nishitani, T., Sakakura, S., and Isoda, T.  
TITLE Human cDNA profile (cDNA) Wakatsuki, A., Oyama, M., Ishii, S.,



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sequence.
ACCESSION  A0142156
VERSION    A0142156.1  GI:11003677
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            ota.T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
            Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
            Isogai, T.
            HRI human cDNA project
            Unpublished (2000)
            Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            16-2-3 Yana, Kasuragi, Chiba 292-0812, Japan
            Tel: 81-438-52-3951
            Fax: 81-438-52-3952

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Email: genomics@helix.jp  
Helix human cDNA project: Genomics Research Institute, Helix  
Research Institute, cDNA Library Construction Department of  
Virology, Institute of Medical Science, University of Tokyo, and  
Helix Research Institute.

#### FEATURES

source  
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clone: "THYR01001863"  
clone\_lib: "THYR01"  
tissue\_type: "thyroid gland"  
note: "Vector: pMT18514"  
BASE COORDINATE: 1 to 767  
ORIGIN: 1 to 767

#### alignment\_scores:

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Ratio: 5.458 Gaps: 1  
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DEFINITION 602628106F1 NC1\_GAP\_Skn4 Homo sapiens cDNA clone IMAGE.4752912 5',  
mRNA sequence.

ACCESSION BC681438 GI:11912835

VERSION 1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 936)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaaps@mail.nih.gov

Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

plate: L1AM10611 row: 1 column: 01

High quality sequence stop: 771

Location/Qualifiers

1..936

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:4752912"

/tissue\_type="squamous cell carcinoma"

/lab\_host="DH10B (T1 phage-resistant)"

/note="organ: skin vector: pMW-Spore6; Site: 1; Not 1;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.5kb. Library constructed by Life

Technologies. Note: this is a NC1\_GAP Library."

BASE COUNT 202 a 296 c 258 g 210 ?

ORIGIN

alignment\_scores:

Quality: 950.50 Length: 207

Ratio: 5.029 Gaps: 4

Percent Similarity: 91.304 Percent Identity: 87.440

alignment\_block:

US-09-525-998a 12 x BC681438

Align seq 1/1 to BC681438 from 1 to 936

1 MetGlySerThrValProAspLeuLeuProLeuValLeuLeuG 17

|||||

229 ATGGGCTGTCCTCCAAATGCCAAGGAAATGCTCAGCTGGAGATCTCTCTTC 278

|||||

17 uLeuLeuValGlyIleTyrProSerGlyValIleGly 29

|||||

270 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 328

|||||

30 .....AspSerValCysProGlnGlyIleTyr 39

|||||

329 TAGGAGACAG 378

|||||

40 HisProGlnAsnAsnSerIleGlyCysThrIleCysAspIleGlySerThrIle 56

|||||

379 CAGCCCTAAAATATTCGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 428

|||||

56 rLeuTyrAsnAspGlySerGlyPheGlyGluAspThrAspGlyGluG 73

|||||

429 CTGTGACAAAGACTGTCTAGGCTCGGAGGAGAGATACGGACCTGAGAGAGAT 478

|||||

73 yScuSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 89

|||||

479 GTAAAG 528

|||||

90 SerCysSerIleCysArgIleValGlyGlnValGlnIleSerSerCys 106

|||||

529 AGCTGCTCCAAATGCCAAGGAAATGCTCAGCTGGAGATCTCTCTTC 578

|||||

106 sThrValAspArgAspThrValCysGlyCysArgLeuLysAsnGlnTyrArg 123

|||||

579 CACATGAG 628

|||||

123 iSyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu 139

|||||

629 ATTATGAG 678

|||||

139 uAsnGlyThrValIleLeuSerCysGlnGlnLysGluAsnThrValCys 156

|||||

679 CAATGGAG 728

|||||

156 hrCysIleAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSer 172

|||||

729 CCTGCATGCAGGTTCTTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 777

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173 AsnCysIleCysSerLeuGluCysThrIleCysLeuProGlnIle 188

|||||

778 AATGAG 827

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189 GluAsnValIleGly 193

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828 CCGAAATCTTCCGCC 842

seq\_name: gb\_est2:BE876920

seq\_documentation\_block:

LOCUS BE876920 971 bp mRNA EST 20-JUL-2000

DEFINITION 601488490F1 NIH-MGC\_69 Homo sapiens cDNA clone IMAGE:4890663 5',

mRNA sequence.

ACCESSION BE876920

VERSION BE876920.1 GI:10355683

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 971)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaaps@mail.nih.gov

Tissue Procurement: Bx15/Dir/Cadaver

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

plate: L1AM9674 row: d column: 24

High quality sequence stop: 722

Location/Qualifiers

1..971

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:4890663"

/tissue\_type="large cell carcinoma, undifferentiated"

/lab\_host="DH10B (phage-resistant)"

/note="organ: lung; vector: pMW-Spore6; Site: 1; Not 1;

Site 2: SalI; Cloned unidirectionally. Primer: oligo dT.

FEATURES

source





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491 AACTGCTGCAAAATGCGAAGAAATGAGTGTGCTGCAAGTGTGAGATGCTGCTTG 540
106 sThrValAspArgAspThrValCysGlyCysArgIysAsnGlnIleThrArgH 123
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541 CACAGCGACGCGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 590
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123 iStyTTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu 139
|||||
591 AATAAGCAGGAAACGCTTCCAGCGGCTGCAATGCGACGCTGCGCCG 540
|||||
140 AsnGlyThrValHisLeuSerCysGlnGluIysGlnAsnThrValCysTh 156
|||||
641 AATGAGAGGCTGCAATGCTGCTGCAATGCTGCTGCAATGCTGCTGCTGCTG 690
|||||
156 rCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSer 172
|||||
691 CTGCAAGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 740
|||||
173 AsnCysLysLysSerLeuGluCysThrLys 182
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741 AACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 771
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seq_name: qb_est2:BE871809

seq_documentation_block:
LOCUS BE871809 969 bp mRNA EST 20-OCT-2000
DEFINITION BE871809 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852525 5',
mRNA sequence
ACCESSION BE871809
VERSION BE871809.1 GI:10320585
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 969)
AUTHORS NIH-MGC http://mgc.nhl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D
Email: cga@biml.nhl.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/INMnet at:
http://image.llnl.gov
plate: L1AM9574 row: 6 column: 22
High quality sequence stop: 642.
location/Qualifiers
1..969
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3852525"
/clone_lib="NIH_MGC_65"
/tissue_type="adenocarcinoma"
/vector="pBMT10 (phage-resistant)"
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies, Inc.

BASE COUNT 281 a 273 c 241 g 174 t
ORIGIN

alignment_scores:
Quality: 94.00 Length: 165
Ratio: 5.671 Gaps: 1
Percent Similarity: 99.94 Percent Identity: 98.788

alignment_block:
us-09-525-998a 12 x BE871809

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Align seq 1/1 to: BE871809 from: 1 to: 969

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37 lysTyrIleHisProGlnAsnAsuSerIleCysCysThrIysCysHisL 54
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2 AAATATATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 51
|||||
53 ysglyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 69
|||||
52 AAGGAACCTACTGTGTACAAATGACTGTCCAGCGCGCGCGCGCGCGCG 101
|||||
70 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuAr 86
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102 TGTAGAGAGTGTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 151
|||||
86 gHisCysLeuSerCysSerLysCysArgIysGluMetGlyGlnValGluI 103
|||||
152 ACACTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 201
|||||
103 leSerSerCysThrValAspArgAspThrValCysGlyCysArgLysAsn 119
|||||
202 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 251
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120 GlnTyrArgHisTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSe 136
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252 CACTAGCGCGCTATTATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 301
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136 rleuCysleuAsnGlyThrValHisleuSerCysGlnGluIysGlnAsn 153
|||||
302 CCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 351
|||||
153 hrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 169
|||||
352 CCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 401
|||||
170 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuFr 186
|||||
402 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 451
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186 gGlnIleGluAsnValIysCylThrGluAspSerCylThr 200
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452 CAGATTGAGAAATGTTAAAGGCTGCTGAGGCTGAGGCTGAGGCTGAG 494
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seq\_name: qb\_est1:AU125680

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seq_documentation_block:
LOCUS AU125680 817 bp mRNA EST 23-OCT-2000
DEFINITION AU125680 NT35M4 Homo sapiens cDNA clone NT35M4005 5', mRNA
sequence.
ACCESSION AU125680
VERSION AU125680.1 GI:10950396
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 817)
AUTHORS Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J.,
Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,T., Sugano,S. and
Isogai,T.
TITLE HRI human cDNA project (Ota,T., Nakamura,A., Ozawa,M., Ishii,S.,
Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki
,Y., Sugano,S., Isogai,T.)
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kasarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5' & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of

```



350 GCGAGACGCGGCGCGCTTCACAGCGCTTCAGAAAACAGCGCTCAGACACAGCGCT 399  
89 uSerCysSerLysCysArgLysGlnMetGlyGlnValGlnValLeuSerSerC 106  
|||||  
400 CAGGAGTCCAAATCCGAAAGGAAATGGGTGAGTGGAGATCTCTT 449  
106 ystThrValAspArgThrValCysGlyCysArgLysAsn.ClnlyrAF 122  
|||||  
450 GCAAGTGGAGCAACAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 499  
122 qHlyTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysL 139  
|||||  
500 GCATTAATGGAGAGAAAAGCTTTCTAGTGGCTTCAATGTGAGCGCTGCGC 549  
139 euAsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCys 155  
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550 TCAATGGAGAGTGCAGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 599  
156 thrCysHisAlaClyPhePheLeuArgGluAsnGluCysValSerCysSe 172  
|||||  
600 AACGTGATGAGATTCTTTCTAAGAGAGAAAGAGTGTGTGTGTGTGTGTGTGTGTGTGT 649  
172 F..... 172  
650 TAGACATCTGCGTGGCGGCGCGCTTCGAAATGGAGTGGGCGGAGATCGCG 699  
172 ..... 172  
700 GTCAATGGAGAGT 749  
173 .....Asn.CysLysLysSerLeuGluCysThrLysL 183  
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750 CCGAAGTAGTGTGGATTACAGCTGTAAAGAAAGCTGTGATTCAGCAAGT 799  
183 eu.CysLeu.ProGlnIleGluAsnValLysGlyThrGluAspSer...G 198  
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800 TGGTCCCTAACCCAGCAATCAGACGTGTAAAGCCGACTTCAGCGAGCTCAGC 849  
198 lyThrThr 200  
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850 GTAGAGCA 857